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Poisson sampling: A sampling strategy for concurrently establishing freedom from disease and estimating population characteristics

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ABSTRACT

Surveys of animal populations are often designed to either demonstrate freedom from disease or to estimate parameters that describe the population, such as disease prevalence, proportion of vaccinated animals, or average animal weight and value. Targeted surveillance is a sampling approach where animals are selected for testing based on the presence of characteristics that indicate a higher probability of disease. This approach can substantially reduce the sample size that is required to demonstrate freedom from disease, but inferences about other population parameters are generally not possible because the sample design often lacks the properties required for making inferences in a traditional survey sample. Determining which animals to sample can also be difficult when either more than one characteristic exists or the characteristic is a continuous attribute, such as age or weight.

Poisson sampling is an unequal probability sampling design that can provide efficiencies similar to targeted surveillance while allowing inferences for other population parameters. The adaptation of Poisson sampling to animal surveys is described. A simulation study, based on sampling a flock of sheep, is used to demonstrate the reductions in sample size that are possible with Poisson sampling. The study showed that the sample size required for a flock-level sensitivity of 0.95 when using Poisson sampling was less than half that required when using simple random sampling. The performance of estimators for prevalence of scrapie and distribution of genotypes are also compared.

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1. Introduction

In both wildlife populations and animal production systems, animals are commonly clustered into groups. Examples of these groups are a herd of beef cattle, a school of fish, a flock of birds, or a consignment of culled animals arriving at slaughter. For simplicity, the general term *group* will be used to describe any collection of animals. Samples are drawn from a group either to substantiate freedom from disease or to estimate characteristics of the group, such as the average weight or market value of animals or the distribution of genotypes. Inferences from the sample may be at the group level (e.g., a herd-accreditation scheme) or at a regional or national level (e.g., the estimation of population parameters, such as the percent of vaccinated animals in a country). In the case of regional or national level inferences, two-stage sampling is often employed; the first stage is selection of a sample of groups and the second stage is the sampling of animals from the group (Cameron and Baldock, 1998b). This study will focus on methods for sampling animals from a group, though the methods can be used for the selection of groups as well.

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Cameron and Baldock (1998a) discuss the need to distinguish between surveys that are designed to demonstrate freedom from disease and those designed to estimate prevalence and other population parameters. This study recognizes the distinction, but focuses on a sampling method for simultaneously meeting both objectives.

Regardless of the objective of the survey, the sampling of animals from a group is almost always necessary. Simple random sampling (SRS) without replacement is generally the standard method for selecting animals from a group. The drawback of this method is that large sample sizes can be required either to substantiate freedom from disease or for precise parameter estimation. In an effort to increase efficiency, a characteristic can be observed for each animal and used to divide the group into subpopulations. The term *subpopulation* will be used to describe any collection of animals whose members all share a common characteristic. It will be assumed that the characteristic is an easily observed ordinal value $x > 0$, such as animal age in years or animal weight. A common approach to increasing statistical efficiency is to divide the sampling effort amongst the subpopulations. This approach forms the basis of both stratified sampling (Cochran, 1977; Särndal et al., 1992) and targeted sampling (Christensen and Gardner, 2000; OIE, 2006; Tavornpanich et al., 2006; Prattley et al., 2007; Williams et al., 2009).

The distinction that we draw between stratified sampling and targeted sampling is that all animals have a nonzero probability of being selected under a stratified design, whereas a targeted sample can be drawn from any subset of the subpopulations (i.e., the user is free to target any number of subpopulations while ignoring others).

Regardless of the sampling method, information about the group is usually required prior to sampling. Some examples include:

- For small groups, or when the prevalence of the disease is low, the total number of animals in the group is required to determine the necessary sample size for establishing freedom from disease (Cameron and Baldock, 1998a, 1998b).
- The construction of a sampling frame is required to implement stratified or fixed-size unequal probability sampling designs.
- When targeted sampling is employed, the number of animals exhibiting a characteristic (e.g., clinical sign) indicating an elevated risk of disease is necessary. Each group is assigned a *point value* and animals are randomly selected from the groups with the highest likelihood of disease. Sampling continues until a predetermined number of points are accumulated.

The need to collect this information prior to sampling can increase the cost and complexity of the survey to the point that a study is not undertaken, or the inferences drawn from the data are restricted (i.e., only freedom from disease can be established).

List-based unequal probability sampling methods can select animals with probability proportional to an easily observed characteristic (also commonly referred to as covariate or auxiliary variable in the sampling literature). In comparison with simple random sampling, the accuracy of the estimators is improved when the characteristic is positively correlated with the parameter of interest. Poisson sampling was introduced by Hajek (1957, 1964) as an unequal probability sampling method that overcomes many of the difficulties associated with fixed-size unequal probability sampling designs. A disadvantage of Poisson sampling is that the sample size is random. However, random sample size designs are already common in disease surveillance applications (OIE, 2006). Särndal (1996) contends that the importance of fixed size designs is over-emphasized, and suggests the use of Poisson sampling on the basis of its ease of implementation and efficiency. Despite its benefits, the use or Poisson sampling is not widespread. An exception is the field of forestry where it is has been a standard method for estimating wood volume in a stand of trees for over 40 years (Grosenbaugh, 1964, 1965; Schreuder et al., 1993; Gregoire and Valentine, 2008).

In this study, Poisson sampling is introduced as an efficient method that allows the determination of disease status and estimation of one or more parameters that describe characteristics of a group of animals. An advantage of Poisson sampling is that it is easily incorporated in any situation where animals are corralled and moved through a chute for processing, as is common practice during vaccination, shearing, blood testing, castration, loading for transportation, or prior to slaughter. The other advantage of Poisson sampling is that the implementation requires nothing more than an estimate of the sum of the characteristic x for all animals in the group. Errors in this estimated total of the characteristic (i.e., $\sum x$) result in a sample size that differs from the originally intended sample size, but no bias is introduced to the estimators.

Various estimators are presented for making inferences about the group. The implementation of Poisson sampling is described first. This is followed by a description of the estimators for group-level attributes of interest (i.e., means, totals and proportions) and demonstrating freedom from disease. An example that mimics the testing of a flock of sheep is used to demonstrate the effectiveness of this technique. A simulation study compares inferences drawn using both Poisson and simple random sampling.

2. Materials and methods

Results for Poisson sampling are presented and contrasted with simple random sampling.

2.1. Drawing a Poisson sample

Suppose a sample of average size n_e is to be drawn from a group of N animals, indexed by i. Associated with each animal is an easily observed ordinal characteristic $x_i > 0$ and M variables of interest $(y_{1i}, y_{2i}, \ldots, y_{Mi})$, about which inferences are to be made. For simplicity assume $M = 1$. The value of x_i will be observed on every animal and y_i will only be observed on sampled animals. If the

total of the characteristic $X = \sum_{i=1}^{N} x_i$ is known prior to sampling and a sample of size n_e is desired, then the probability of including the animal in a Poisson sample is defined by

$$p(\text{animal } i \text{ is sampled}) = \pi_i = \frac{n_e x_i}{X}.$$

Suppose animals are run through a chute. To select a Poisson sample, a random number $r_i \sim Uniform(0, 1)$ is generated for each animal i and it is selected if $r_i < \pi_i$. The variables of interest y_i are measured for each selected animal. Poisson sampling is a draw-by-draw procedure where the achieved sample size, n, is random. On average, the sample size is $E[n] = \sum_{i=1}^{N} \pi_i = n_e$.

Note that the implementation of Poisson sampling, as described in most sampling texts (Särndal et al., 1992), assumes that X is known. This would require that x_i be observed for each animal prior to sampling and would render Poisson sampling impractical for this application. To avoid this problem, an estimate of the total $\tilde{X}$ can be used. To illustrate, consider the following example. Assume that a consignment of culled animals is gathered in a pen at an abattoir and that we would like to estimate some population-level parameter, such as a mean or total of the variable of interest y. Also assume that the weight of the animal (x_i) is a characteristic that is known to be correlated with the variable of interest (y_i).[2] Assume that it is estimated that the pen contains approximately 110 animals and that past experience suggests that the average weight of culled animals is 120 kg. Let $\tilde{X} = 110 \times 120 = 13200$ and suppose a sample of $\tilde{n}_e = 30$ animals is desired, where the $\sim$ denotes that these values are initial estimates chosen prior to sampling. For each animal that enters the chute, the actual weight (x_i) is recorded and a random number, $r_i \sim Uniform(0, 1)$, is generated. The animal is selected for measurement if $r_i < \tilde{n}_e x_i / \tilde{X}$. After all animals have exited the chute, the y value will have been observed on n animals and the true total weight (X) is known. Then the true anticipated sample size can be adjusted using $n_e = \tilde{n}_e X / \tilde{X}$ and the actual inclusion probability for each animals is calculated as $\pi_i = n_e x_i / X$.

In some situations, it is either necessary or desirable to select animals regardless of the size of the characteristic x. For example, samples may be required from all animals that exhibit central nervous system disorders because of the public health concerns related to rabies. These same animals are desirable for surveillance applications because central nervous system disorders indicate a high likelihood of scrapie or bovine spongiform encephalopathy. Poisson sampling accommodates this situation by simply setting the inclusion probability for these animals to $\pi_i = 1$. If animal i is to be selected with certainty, then both the expected sample size and total of the characteristic are adjusted by $n_e^{adj} = n_e - 1$ and $X^{adj} = X - x_i$ to account for the fact that a sample of average size n_e^{ave} will be drawn from the remaining $N - 1$ animals.

[2] The motivation for this correlation will be provided with the description of the estimator.

2.2. Estimators of population totals, means and proportions

A number of different estimators have been proposed for use in conjunction with Poisson sampling (Magnussen, 2002 and references therein). The most commonly used estimator for the total is

$$\hat{Y}_{Pois} = \frac{n_e}{n} \sum_{i=i}^{n} \frac{y_i}{\pi_i},$$

where n is the actual number of animals samples. An approximate variance estimator is

$$\text{var}[\hat{Y}_{Pois}] = \left(1 - \frac{n_e}{N}\right) \left(\frac{1}{n_e(n-1)}\right) \sum_{i=i}^{n} \left(\frac{n_e y_i}{\pi_i} - \hat{Y}_{Pois}\right)^2. \quad (1)$$

In the development of Poisson sampling given above, it was mentioned that the characteristic x_i is chosen so that it is positively correlated with y_i. To motivate this requirement, note that if x_i and y_i are perfectly correlated (i.e., $y_i = \kappa x_i$), the resulting Poisson sampling estimator has zero variance because for any sample

$$\hat{Y}_{Pois} = \frac{n_e}{n} \sum_{i=i}^{n} \frac{y_i}{\pi_i} = \frac{n_e}{n} \sum_{i=i}^{n} \frac{\kappa x_i X}{n_e x_i} = Y.$$

This result also demonstrates that transformations of the characteristic should be considered if a transformation would result in a linear relationship between x_i and y_i. An example of such a transformation is $x_i = \sqrt[3]{\text{animal weight}}$. The estimators for Poisson sampling are still valid when y_i and x_i are uncorrelated, but the variance of $\hat{Y}_{Pois}$ is generally larger than the variance achieved by a simple random sample.

If a sample of size $n = n_e$ is drawn using simple random sampling with replacement, the estimator of the total is given by

$$\hat{Y}_{SRS} = \frac{N}{n} \sum_{i=i}^{n} y_i$$

with variance estimator

$$\text{var}[\hat{Y}_{SRS}] = \left(1 - \frac{n}{N}\right) \frac{1}{n(n-1)} \sum_{i=i}^{n} (y_i - \bar{Y}_{SRS})^2. \quad (2)$$

Estimators of the mean or proportion are

$$\bar{Y}_{Pois} = \frac{\hat{Y}_{Pois}}{N}$$

and

$$\bar{Y}_{SRS} = \frac{\hat{Y}_{SRS}}{N}.$$

Additional results and a detailed summary of Poisson sampling are given by Gregoire and Valentine (2008).

2.3. Demonstrating freedom from disease

The use of unequal probability list-based sampling designs has not been discussed in relation to applications where the goal is demonstrating freedom from disease. A short discussion follows in order to introduce notation: Suppose the objective of a study is to show that p(the level of disease in the population is $< P_D$) $\geq 1 - \alpha$, where P_D is the

prevalence considered sufficiently low to consider the population effectively free of the disease (i.e., the design prevalence). The probability of sampling a healthy animal at random is $p(\text{the animal is healthy}) = (1 - P_D)$. In situations where $N \gg n$, this result can be extended to a simple random sample of n animals so that $p(\text{all sampled animals are healthy}) \approx (1 - P_D)^n$. Then $p(1 \text{ or more disease animal sampled}) = 1 - p(\text{all sampled animals are healthy} \approx 1 - (1 - P_D)^n$. This approximate solution holds for situations where the sample size is such that $n/N \lesssim 0.1$. A smaller sample size can be used when the sampling fraction exceeds about 10% (Cameron and Baldock, 1998a).

Targeted sampling is an approach where samples are drawn from specific subpopulations, much like stratified sampling. Targeted sampling differs from traditional stratified sampling, however, because samples need not be drawn from all subpopulations to make inferences about disease freedom (e.g., OIE, Terrestrial Animal Health Code [Article 3.8.1.6]).

The underlying concept of targeted sampling is that it is possible to increase the prevalence in the part of the population from which samples are drawn, which reduces the required sample size. This is accomplished by dividing the population into subpopulations where the prevalence in one of the subpopulations is higher than the prevalence in the general population. In this subpopulation there is a higher probability of finding disease in any sampled animal.

The connection between Poisson sampling and targeted sampling is made through the use of the characteristic x_i to determine whether the animal is sampled. Suppose there is an objective risk factor for the disease that is related to the value of the x. For the sake of simplicity assume the characteristic has two levels; presence (C) and absence ($\bar{C}$). The characteristic is used to divide the population into two subpopulations, with disease prevalence in each subpopulation being P_C and $P_{\bar{C}}$. Each animal in each subpopulation is given a *point value*. This point value is $\gamma = 1$ for animals that are randomly chosen from the general population. Animals that exhibit the characteristic C have a higher probability of being diseased and are assigned a point value greater than 1. The relationship between the point value and the prevalence of disease for animals exhibiting the characteristic is $P_C = \gamma P_D$, where γ is greater than one for animals in the targeted subpopulation and γ relates the prevalence in the targeted subpopulation to the prevalence in the general population. Animals without the characteristic are assigned a point value less than 1. An intuitive interpretation is that each animal from the targeted subpopulation is "worth" γ randomly chosen animals from the general population. If the point value for an animal is γ then

$$1 - \alpha = 1 - (1 - P_D)^n \approx 1 - (1 - P_C)^{n/\gamma}.$$

This definition of γ sets the relationship between overall design prevalence and the design prevalence in the targeted subpopulation and assumes these values would be known. While this information is usually not known, the point values can also be derived from the risk ratio associated with the characteristic and knowledge of the proportion of the population exhibiting the characteristic x. These values are often provided in studies describing the epidemiology of the disease and the population under study. Williams et al. (2009) provide the derivations for determining point values from the epidemiologic characteristics of the disease.

Demonstrating freedom from disease with data from a Poisson sample is a straightforward adaptation of targeted sampling. It assumes that the relationship between the design prevalence in a subpopulation, defined by the characteristic x, and the general population can be determined. The point value associated with the characteristic will be denoted $\gamma(x_i) = P_{C(x_i)}/P_D$, where $P_{C(x_i)}$ is the prevalence in the subpopulation defined by x_i. Then the probability of a Poisson sample containing one or more diseased[3] animals when the level of disease is P_D is

$$p(\text{detecting disease}) = HSe \approx 1.0 - \prod_{i=1}^{n}(1 - \gamma(x_i)P_D). \quad (3)$$

This approximation assumes an infinite population. It is a conservative estimator of the level of confidence for smaller populations.

When the characteristic, x, takes on K different discrete values, such as animal age in years, the hypergeometric distribution can be used to provide an exact confidence. The confidence achieved for discrete x values is

$$p(\text{detecting disease}) = HSe = 1.0 - \prod_{k=1}^{K} f(0; N_k, P_{C_k}, n_k), \quad (4)$$

where N_k is the number of animals in class k, P_{C_k} is the prevalence in subpopulation k, n_k is the number of animals chosen from subpopulation k by Poisson sampling, and

$$f(0; N_k, \gamma(x_k)P_D, n_k) = \frac{\binom{N_k\gamma(x_k)P_D}{0}\binom{N_k(1-\gamma(x_k)P_D)}{n_k}}{\binom{N_k}{n_k}},$$

is the probability mass function of the hypergeometric distribution and assumes that $N_k\gamma(x_k)P_D$ is an integer value.

In the context of two-stage sampling, $HSe = p(\text{detecting disease})$ is the group or herd-level sensitivity. If $j = 1, \ldots, J$ groups are sampled, the system-level sensitivity is

$$SSe = 1 - \prod_{j=1}^{J}(1 - P_{Dherd}HSe_j),$$

where P_{Dherd} is the design herd prevalence and HSe_j is the herd-level sensitivity for group j.

Note that Eqs. (3) and (4) reduce to the standard equations for estimating HSe with simple random sampling when $\gamma(x_i) = 1$ and $K = 1$. The estimators presented above also assume a perfect test is used. While this is never the case, the appropriate adjustments to account for the sensitivity and specificity of the test, or tests, depends on whether test-positive animals receive further investigation to validate the presence of disease in the animal.

[3] Disease is arbitrarily chosen as the condition of interest. This development could equally apply to infection, carrier status or some other case definition.

Results from Cameron and Baldock (1998a, 1998b) and Cannon (2002) can be used to adjust the *HSe* values given in Eqs. (3) and (4) to account for test sensitivity and specificity.

Both Eqs. (3) and (4) assume that the risk ratio associated with the characteristic is a value that is known with certainty. This assumption is common in most if not all of the current targeted surveillance applications (e.g., bovine spongiform encephalopathy surveillance as described in OIE, 2006). These values are never actually known with certainty. Methods for incorporating this source of uncertainty are described in Williams et al. (2009).

2.4. Population description

Three data sets, representing sheep flocks of various sizes, were constructed for the purpose of illustration. The purpose for creating different flocks was to illustrate the effect of population size on the approximation used to derive Eq. (3). Populations consisting of $N = 100$, 200 and 300 animals were created.

The populations were constructed to demonstrate the use of Poisson sampling to concurrently demonstrate freedom from disease and estimate the mean of five variables of interest ($y_1, y_2, \ldots, y_5$). The first four variables of interest are indicators of presence/absence that are only weakly associated with the x characteristic. The remaining variable of interest is ordinal and highly correlated with the characteristic (x) used to determine animal selection. This will demonstrate the spectrum of possible efficiency gains and losses associated with Poisson sampling.

The populations used in the simulation study were based on data collected by the Scrapie Slaughter Surveillance program in the U.S., with the information being derived from the testing of sheep flocks found positive for scrapie through slaughter surveillance. For each of the 2300 animals, information on animal age and genotype were available, while the results of a third eyelid test (O'Rourke et al., 2000) for scarpie was recorded on those animals deemed susceptible for scrapie as a results of the genetic testing.

Scrapie is a fatal neurodegenerative disease of sheep and goats. Animals are thought to be most susceptible to scrapie infection at a young age (Baylis et al., 2002), with the epidemiology of the disease such that the peak incidence occurs in animals between 2 and 3 years of age (Redman et al., 2002). The epidemiology of scrapie is such that the risk of disease changes with animal age. The age distribution of infected animals is expected to differ from the overall age distribution, with the age distribution for infected animals shifted to the left. This is depicted in Fig. 1. Animal age is a logical characteristic to use that will focus sampling on higher prevalence subpopulations. In order to implement Poisson sampling, so that younger animals have a higher probability of selection, the characteristic

$$x_i = \frac{1}{\text{age of animal } i \text{ in years}},$$

was chosen.

Reported flock-level prevalence for scrapie varies from as little as 2% to in excess of 40%. These differences are largely attributed to differences in the fraction of genetically susceptible animals (Redman et al., 2002) and the time since introduction of the disease. The data set contained 24 infected animals out of 300, for a prevalence of 0.08. The prevalence of scrapie-infected sheep was the first population parameter of interest. To estimate the prevalence, the value

$$y_{1i} = \begin{cases} 1 & \text{if animal } i \text{ has scrapie} \\ 0 & \text{otherwise} \end{cases}$$

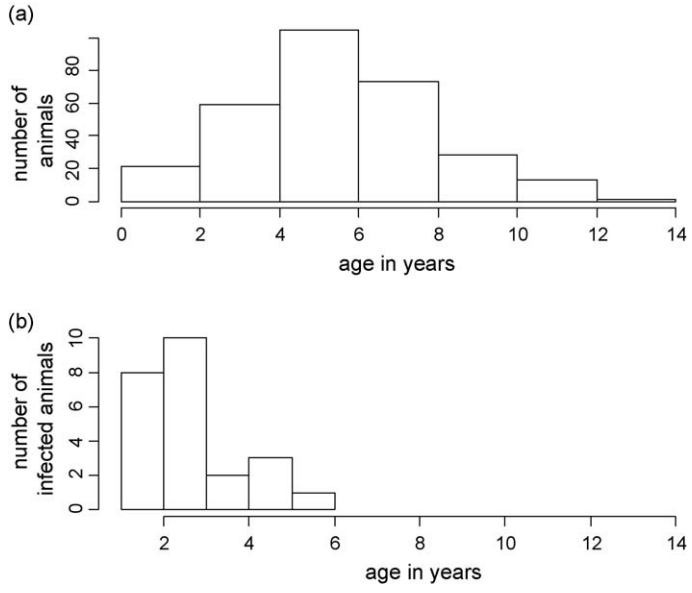

Fig. 1. The top histogram (a) displays the age distribution for the flock of $N = 300$ sheep. The bottom histogram (b) shows the age distribution for scrapie-infected animals.

was recorded for every animal selected by either Poisson or simple random sampling.

Susceptibility to scrapie has been linked to specific polymorphisms in the PrP protein associated with codons 136, 154 and 171. The scrapie eradication program in the United States has found that the vast majority of scrapie-infected sheep are genotype *QQ* on codon 171, while no positive animals have been found with the allele *RR* and are assumed highly resistant. The distribution of genotypes was (14.8, 39.3, 45.9%) for the *QQ*, *QR*, and *RR* genotypes. To estimate the proportion of the flock with the *QQ* genotype, the value

$$y_{2i} = \begin{cases} 1 & \text{if animal } i \text{ was } QQ \\ 0 & \text{otherwise} \end{cases}$$

was recorded for each animal selected by either Poisson or simple random sampling. Similar definitions of y_{3i} and y_{4i} were made to estimate the proportion of the flock with the *QR* and *RR* genotype.

The population parameter y_{5i} was artificially generated; with its purpose being to demonstrate the efficiency of Poisson sampling when the x and y values are correlated.

The y_{5i} values were created so that $y_{5i} = \beta x_i + \varepsilon$, with ε having mean 0 and increasing variance, as is common in many biological phenomena. Fig. 2 depicts the relationship between y_{5i} and x_i. Such a relationship is expected to exist when describing an animal's value in terms of characteristics such as meat quality or monetary value as breeding stock because these characteristics decrease with an animal's age. An example of this type of relationship is Woodward et al. (2000), where ante-mortem muscle tissue biopsies were collected to assess meat quality. The term *meat quality* metric and the abbreviation *MeatQ* will be used to refer to y_{5i}.

Point values are required for demonstrating freedom from disease. The point values are 1 for simple random sampling, while the integration of targeted sampling and Poisson sampling requires that γ values be described as functions of the inverse of animal age. The values used in this example are based on the actual prevalence in each age class and the population prevalence, and are given by $\gamma(x = 1) = 5.62$, $\gamma(x = 1/2) = 4.89$, $\gamma(x = 1/3) = 3.41$, $\gamma(x = 1/4) = 1.85$, $\gamma(x = 1/5) = 0.58$, $\gamma(x = 1/6) = 0.22$, $\gamma(x = 1/7) = 0.08$, $\gamma(x > 1/7) = 0$.

Note that no specific functional relationship is required between the point values and animal age. The purpose of Poisson sampling is to provide a probabilistic sample of animals that are at higher risk of disease than would be achieved by simple random sampling. The value of this sample, in terms of demonstrating freedom from disease, is determined strictly through the epidemiologic properties of the disease as they relate to the characteristic x.

2.5. Simulation study

The simulation study was run for a range of anticipated sample sizes from $n_e = 10$ to 60. For each anticipated sample size, 20,000 realizations of Poisson and simple random sampling were drawn from the flock. For each realization, the scrapie status, genotype and meat quality metric was recorded for each sampled animal. From these data, the number of infected animals, the proportion of animals with each genotype, and the average meat quality was estimated using Eqs. (1) and (2). Whether an infected animal was found among the sample was also recorded. Then the flock-level sensitivity of the two sampling designs was estimated by

$$HSe = \frac{\text{number of realizations where a positive was found}}{20,000}.$$

This value was compared against the calculated confidence levels given in Eqs. (3) and (4).

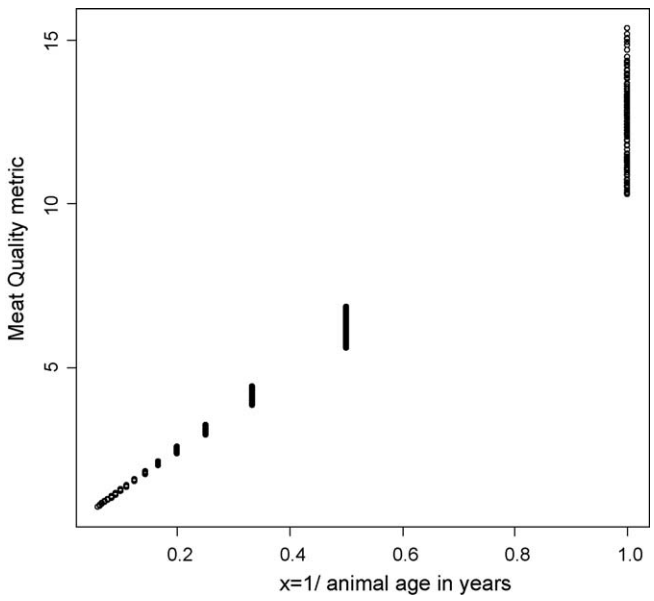

Fig. 2. Relationship between the characteristic x_i and the meat quality metric y_{5i}. This artificially generated relationship is used to demonstrate a situation where Poisson sampling would be highly efficient in comparison to simple random sampling.

To compare Poisson and simple random sampling, the relative efficiency metric

$$RE_* = \frac{\sqrt{V[\hat{Y}_{SRS}]}}{\sqrt{V[\hat{Y}_{Pois}]}}$$

was used, where * indicates which population parameter was estimated (i.e., prevalence, proportion of animals with QQ, QR, RR genotypes, and the meat quality metric (*MeatQ*)). This metric expresses how many times larger the standard error of the simple random sampling estimator was when compared to $\hat{Y}_{Pois}$. The advantage of using *RE* to compare estimators is that the number of samples required to achieve equal variance with simple random sampling, denoted by n_{EV}, is calculated as $n_{EV} = nRE^2$.

Results are reported for the $n_e = 25$ sample size.

3. Results

The flock-level sensitivity, as a function of anticipated sample size, is given in Fig. 3a and b, for the $N = 100$ and 300 data sets ($N = 200$ not shown). The sensitivity derived from Poisson sampling was substantially higher than that of simple random sampling across the range of sample

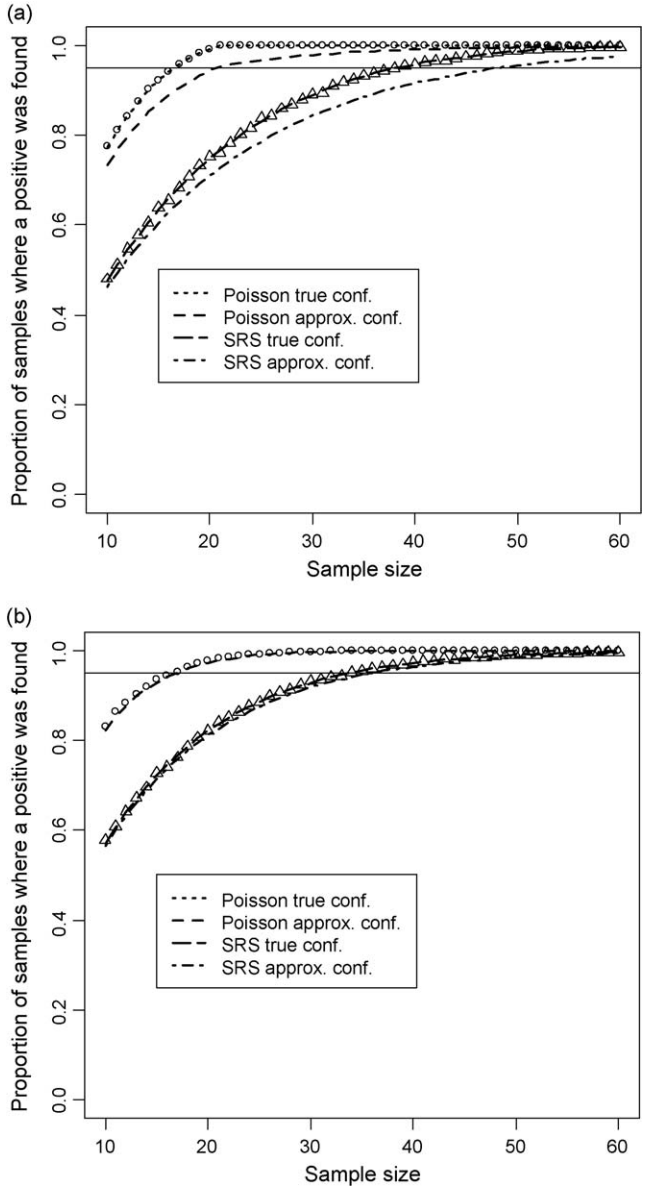

Fig. 3. The proportion of samples where at least one infected animal was sampled from a when a sample of size n_e was drawn from the population using Poisson or SRS sampling. Figures (a) and (b) correspond to population sizes of $N = 100$ and 300 animals, respectively. The dashed lines represent the calculated probability of sampling one or more positives animals given in Eqs. (3) and (4). The small circles ○ and triangles △ illustrate the Monte Carlo simulation values and verify the results of Eq. (4).

Table 1
The performance metrics used for comparing Poisson sampling to simple random sampling without replacement. The relative efficiency metrics, RE_*, describes how many times larger the sample size for simple random sampling must be in order to achieve an equal sampling error to Poisson sampling. The $n_e(95)$ and $n(95)$ values give the minimum sample size required to be 95% confident of sampling at least one positive animal for the each of the three flock sizes.

Population size	$RE_{prevalence}$	RE_{QQ}	RE_{QR}	RE_{RR}	RE_{MeatQ}	Poisson sample size n_e (95)	SRS sample size n (95)
$N = 100$	1.52	0.82	0.74	0.83	30.8	17	38
$N = 200$	1.32	0.96	0.77	0.81	20.2	15	31
$N = 300$	1.30	0.95	0.77	0.82	19.4	17	34

sizes. Sensitivity for Poisson sampling reached 95.0% with anticipated sample sizes ranging from $n_e = 15$ to 17 and exceeded 99% for as few as $n_e = 20$ samples. In contrast, the sensitivity of simple random sampling reached 95% for sample sizes that ranged from 31 to 38 animals and required approximately 50 samples before exceeding 99% confidence.

The approximate confidence formula, given in Eq. (3), consistently underestimated the true confidence for the population consisting of $N = 100$ animals (Fig. 3a). The difference between the approximate and true confidence levels was almost indistinguishable for the larger population (Fig. 3b).

The Poisson sampling estimator had a smaller variance when estimating the prevalence of scrapie (Table 1). The relative efficiency ranged from $RE_{prevalence} = 1.30–1.52$, so a survey based on simple random sampling would require approximately 30–52% more samples than an equivalent survey that used Poisson sampling to obtain parameter estimates with the same sampling error. In contrast, the simple random sampling estimator had a smaller variance when estimating the proportion of animals with each genotype. The relative efficiencies, given in Table 1, ranged from $RE_{QQ} = 0.82–0.95$, $RE_{QR} = 0.74–0.77$, and $RE_{RR} = 0.80–0.83$. The relative efficiency was less than 1 for these parameters because the association between the animal age and genotype was low for each data set.

Estimation of the meat quality metric illustrates the potential efficiency gains associated with Poisson sampling under nearly ideal conditions. The range of relative efficiencies, given in Table 1 was $RE_{MeatQ} = 19.4–30.8$. This increase in efficiency suggests that, in the worst case, a Poisson sample of size of approximately 2 animals has the same inferential power as a simple random sample of size approximately 40. It is unknown whether this result is representative of any realistic application in animal populations. Linear relationships with this degree of correlation exist in many natural resource populations (e.g., Gregoire and Valentine, 2008, Chapter 3) and dramatic improvements in statistical efficiency have been reported when using Poisson sampling. We suspect that similar relationships may exist between characteristics such as live-animal weight (x) and monetary value or net product weight (y).

4. Discussion

Many applications in animal surveillance, including targeted surveillance, are based on the assumption that a simple random sample is drawn from either the population, or an appropriate subpopulation, in the case of stratified random sampling. Nevertheless, drawing such samples requires constructing a sampling frame that identifies each animal prior to sampling. In practice, most surveys use either an opportunistic or systematic sample and assume that the realized sample is sufficiently similar to a simple random sample that the associated estimators will provide reasonable approximations. In contrast, sampling strategies based on Poisson sampling do not require any assumptions about the adequacy of such approximations because the sampling design is well defined (i.e., Poisson sampling is a measurable design as described by Särndal et al., 1992) and it is these properties that allow the concurrent estimation of parameters other than the prevalence of the disease. One way to view Poisson sampling is that it is allows for samples to be drawn while the frame is being constructed.

While this study has focused on methods for sampling animals from a group, the same methodology could be applied to selecting groups of animals with unequal probability. For example, one might select groups of deer for *tuberculosis* testing based on the group's distance from an infected cattle herd.

The results of the simulation study are somewhat mixed, with Poisson sampling performing very well for the detection of disease and estimation of prevalence and the meat quality metric, but simple random sampling was superior for determining the distribution of genotypes. This is a common problem when designing any type of survey where there is interest in making inferences about multiple population parameters. The key advantages of Poisson sampling are that it can focus the sampling effort on animals of high interest, yet still allows for inference on multiple parameters, though the parameter estimates for population parameters that are not correlated with the characteristic x are likely to be imprecise.

The primary drawbacks of Poisson sampling for disease surveillance are the random sample size, the inability to specify a fixed confidence level prior to sampling, and the method's reliance on values which may be difficult to acquire, such as the risk ratio associated with a characteristic, for the calculation of $\gamma(x_i)$. Williams et al. (2009) provide results that account for these unknown values based on the epidemiological properties of the disease. Another reasonable solution is to choose conservative values for the point values associated with each sampled animal.

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